

SEQUENCE LISTING

<110> Istituto Superiore di Sanità
National Institutes of Health

<120> COLORECTAL ANTIGEN

<130> WPP88367

<150> US 60/512,040

<151> 2003-10-15

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1413

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85)..(1395)

<220>

<221> misc_feature

<222> (1180)..(1240)

<223> nucleotide sequence encoding the immunogenic peptide

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cctgcatccc atgactcgga gctg atg gcc ttc atg acg agg aag ttg tgg 111
Met Ala Phe Met Thr Arg Lys Leu Trp
1 5

gac ctg gag cag cag gtg aag gcc cag act gat gag ata ctg tcc aag 159
Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu Ile Leu Ser Lys
10 15 20 25

gat cag aag ata gcg gcc cta gag gac ctg gtg cag acc ctc cgg cca 207
Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln Thr Leu Arg Pro
30 35 40

cac cca gcc gag gca acc ctg cag cgg cag gag gaa ctg gag acg atg 255
His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu Leu Glu Thr Met
45 50 55

tgt gtg cag ctg cag cgg cag gtc agg gag atg gag cgg ttc ctc agt 303
Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu Arg Phe Leu Ser
60 65 70

gac tat ggc ctg cag tgg gtg ggc gag ccc atg gac cag gag gac tca 351
Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu Asp Ser
75 80 85

gag agc aag aca gtc tca gag cat ggc gag agg gac tgg atg aca gcc 399
Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met Thr Ala
90 95 100 105

aag aag ttc tgg aag cca ggg gac tca ttg gcg ccc cct gag gtg gac 447
Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu Val Asp
110 115 120

ttt gac agg ctg ctg gcc agc ctg cag gat ctt agt gag ctg gtg gta 495
Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu Val Val

125	130	135	
gag ggt gac acc caa gtg aca cca gtg ccc ggc ggg gca cgg ctg cgt Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg Leu Arg 140 145 150			543
acc ctc gag ccc atc ccg ctg aag ctc tac cgg aat ggc atc atg atg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile Met Met 155 160 165			591
ttc gac ggg ccc ttc cag ccc ttc tac gat ccc tcc aca cag cgc tgc Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln Arg Cys 170 175 180 185			639
ctc cga gac ata ttg gat ggc ttc ttt ccc tca gag ctc cag cga ctg Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln Arg Leu 190 195 200			687
tac ccc aat ggg gtc ccc ttt aag gtg agt gac ttg cgc aat cag gtc Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn Gln Val 205 210 215			735
tac ctg gag gat gga ctg gac ccc ttc cca ggc gag ggc cgt gtg gtg Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg Val Val 220 225 230			783
ggc agg cag cgg atg cac aag gcc ttg gac agg gtg gag gag cac cca Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu His Pro 235 240 245			831
ggc tcc agg atg act gct gag aaa ttt ctg aac agg ctc ccc aag ttt Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro Lys Phe 250 255 260 265			879
gtg atc cgg caa ggc gag gtg att gac atc cgg ggc ccc atc agg gac Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile Arg Asp 270 275 280			927
acc ttg cag aac tgc tgc cca ttg cct gcc cgg atc cag gag att gtg Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu Ile Val 285 290 295			975
gtg gag acg ccc acc ttg gcc gct gag cga gag agg agc cag gag tca Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln Glu Ser 300 305 310			1023
ccc aac aca ccg gca ccc ccg ctc tcc atg ctg cgc atc aag tct gag Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys Ser Glu 315 320 325			1071
aat ggg gaa cag gcc ttc cta ctg atg atg cag cct gac aac acc att Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn Thr Ile 330 335 340 345			1119
ggg gac gtg cga gct ctg cta gcg cag gcc agg gtc atg gat gcc tct Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser 350 355 360			1167
gcc ttt gag atc ttc agc aca ttc ccg ccc acc ctc tac cag gac gat Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp 365 370 375			1215
aca ctc acg ctg cag gct gca ggc ctt gtg ccc aaa gca gca ctg ctg Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu 380 385 390			1263
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<400> 2

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Ala Gln Thr Asp Glu Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu
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Glu Asp Leu Val Gln Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu
35 40 45

Gln Arg Gln Glu Glu Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln
50 55 60

Val Arg Glu Met Glu Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val
65 70 75 80

Gly Glu Pro Met Asp Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu
85 90 95

His Gly Glu Arg Asp Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly
100 105 110

Asp Ser Leu Ala Pro Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser
115 120 125

Leu Gln Asp Leu Ser Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr
130 135 140

Pro Val Pro Gly Gly Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu
145 150 155 160

Lys Leu Tyr Arg Asn Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro
165 170 175

Phe Tyr Asp Pro Ser Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly
180 185 190

Phe Phe Pro Ser Glu Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe
195 200 205

Lys Val Ser Asp Leu Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp
210 215 220

Pro Phe Pro Gly Glu Gly Arg Val Val Gly Arg Gln Arg Met His Lys
225 230 235 240

Ala Leu Asp Arg Val Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu
245 250 255

Lys Phe Leu Asn Arg Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val
260 265 270

Ile Asp Ile Arg Gly Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro
275 280 285

Leu Pro Ala Arg Ile Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala
290 295 300

Ala Glu Arg Glu Arg Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro
305 310 315 320

Leu Ser Met Leu Arg Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu
325 330 335

Leu Met Met Gln Pro Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu
340 345 350

Ala Gln Ala Arg Val Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr
355 360 365

Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala
370 375 380

Gly Leu Val Pro Lys Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro
385 390 395 400

Lys Ser Ser Leu Lys Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro
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Gly Pro Ser Pro Gly Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro
420 425 430

Ser Pro Ser Pro Gln
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<211> 60
<212> DNA
<213> Homo sapiens

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<210> 4
<211> 20
<212> PRT
<213> Homo sapiens

<400> 4

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Gln Ala Ala Gly
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<210> 5
<211> 42
<212> DNA
<213> Homo sapiens

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accctctacc aggacgatac actcacgctg caggctgcag gc 42

<210> 6
<211> 14
<212> PRT
<213> Homo sapiens

<400> 6

Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly
1 5 10

<210> 7
<211> 1028
<212> DNA
<213> Homo sapiens

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ggggactcat tggcgcccc tgaggtggac tttgacaggc tgctggccag cctgcaggat 180
cttagtgagc tgggtgtaga gggtgacacc caagtgcacac cagtgcccg cggggcacgg 240
ctgcgtaccc tcgagcccat cccgctgaag ctctaccgga atggcatcat gatgttcgac 300
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gacttgcgca atcaggtcta cctggaggat ggactggacc ccttcccagg cgagggccgt 480
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 <212> PRT
 <213> Homo sapiens

<400> 8

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Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu
 35 40 45

Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu
 50 55 60

Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg
 65 70 75 80

Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile
 85 90 95

Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln
 100 105 110

Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln
 115 120 125

Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn
 130 135 140

Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg
 145 150 155 160

Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu
 165 170 175

His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro
 180 185 190

Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile
 195 200 205

Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu
 210 215 220

Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln
 225 230 235 240

Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys
 245 250 255

Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn
 260 265 270

Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp
 275 280 285

Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln
 290 295 300

Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala
 305 310 315 320

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 325 330 335

Pro Gly Pro Cys Pro Gly Pro
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<210> 9
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 9

Phe Ser Thr Phe Pro Pro
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<210> 10
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 10

Leu Val Pro Lys Ala Ala
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<210> 11
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 <212> DNA
 <213> Homo sapiens

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 ttcagtcctg gtccctgtcc cgggtcccggt cccggcccca gtcccgggtcc cgggtcccggc 240
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<210> 12
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 <212> PRT
 <213> Homo sapiens

<400> 12
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 Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp
 20 25 30
 Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu
 35 40 45
 Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly
 50 55 60
 Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly
 65 70 75 80
 Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
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<210> 13
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 <212> DNA
 <213> ARTIFICIAL

<220>
 <223> PCR primer sequence

<400> 13
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<210> 14
 <211> 18
 <212> DNA
 <213> artificial

<220>
 <223> PCR primer sequence

<400> 14
 ccttgaatgt ggtcatct 18

<210> 15
<211> 23
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<213> artificial

<220>
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<400> 15
cgtttcttgg agtactctac gtc

23

<210> 16
<211> 20
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<210> 17
<211> 20
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<400> 17

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Gln Ala Ala Gly
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<210> 18
<211> 20
<212> PRT
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<400> 18

Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val
1 5 10 15

Pro Lys Ala Ala
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<210> 19
<211> 1771
<212> DNA
<213> Homo sapiens

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aggagcaggc agataacaga aacttccaga aacctctgtg gagacagtgg aagaggcaaa 180
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tagcaagacc cgaaaagtgc ccttgccctc ggagcctatg aatcctggga ggcgaggaat 300
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 tccagcccc caataaagca ccgccccct c 1771

<210> 20
 <211> 512
 <212> PRT
 <213> Homo sapiens

<400> 20

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Asp Glu Asp Glu Val Asp Met Leu Ser Asp Gly Cys Gly Ser Glu Glu
 35 40 45

Lys Ile Ser Val Pro Ser Cys Tyr Gly Gly Ile Gly Ala Pro Val Ser
 50 55 60

Arg Gln Val Pro Ala Ser His Asp Ser Glu Leu Met Ala Phe Met Thr
 65 70 75 80

Arg Lys Leu Trp Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu
 85 90 95

Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln
 100 105 110

Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu
 115 120 125

Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu
 130 135 140

Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp
 145 150 155 160

Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp
 165 170 175

Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro
 180 185 190

Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser
 195 200 205

Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly
 210 215 220

Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn
 225 230 235 240

Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser
 245 250 255

Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu
 260 265 270

Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu
 275 280 285

Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu
 290 295 300

Gly Arg Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val
305 310 315 320

Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg
325 330 335

Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly
340 345 350

Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile
355 360 365

Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg
370 375 380

Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg
385 390 395 400

Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro
405 410 415

Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val
420 425 430

Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu
435 440 445

Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys
450 455 460

Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys
465 470 475 480

Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly
485 490 495

Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
500 505 510